Full wwPDB X-ray Structure Validation Report ⓘ

Jul 12, 2021 – 11:08 pm BST

PDB ID	:	6YMT
Title	:	RNASE 3/1 version1
Authors	:	Fernandez-Millan, P.; Prats-Ejarque, G.; Vazquez-Monteagudo, S.; Boix, E.
Deposited on	:	2020-04-09
Resolution	:	1.58 Å(reported)

This is a Full wwPDB X-ray Structure Validation Report for a publicly released PDB entry.

We welcome your comments at *validation@mail.wwpdb.org*
A user guide is available at
https://www.wwpdb.org/validation/2017/XrayValidationReportHelp
with specific help available everywhere you see the ⓘ symbol.

The following versions of software and data (see references ⓘ) were used in the production of this report:

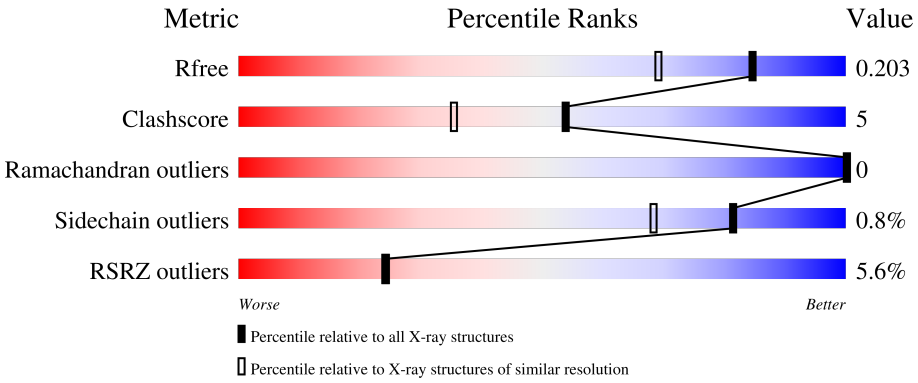
MolProbity	:	4.02b-467
Mogul	:	1.8.5 (274361), CSD as541be (2020)
Xtriage (Phenix)	:	1.13
EDS	:	2.22
Percentile statistics	:	20191225.v01 (using entries in the PDB archive December 25th 2019)
Refmac	:	5.8.0158
CCP4	:	7.0.044 (Gargrove)
Ideal geometry (proteins)	:	Engh & Huber (2001)
Ideal geometry (DNA, RNA)	:	Parkinson et al. (1996)
Validation Pipeline (wwPDB-VP)	:	2.22

1 Overall quality at a glance (i)

The following experimental techniques were used to determine the structure:
X-RAY DIFFRACTION

The reported resolution of this entry is 1.58 Å.

Percentile scores (ranging between 0-100) for global validation metrics of the entry are shown in the following graphic. The table shows the number of entries on which the scores are based.



Metric	Whole archive (#Entries)	Similar resolution (#Entries, resolution range(Å))
R_{free}	130704	5534 (1.60-1.56)
Clashscore	141614	5861 (1.60-1.56)
Ramachandran outliers	138981	5708 (1.60-1.56)
Sidechain outliers	138945	5703 (1.60-1.56)
RSRZ outliers	127900	5431 (1.60-1.56)

The table below summarises the geometric issues observed across the polymeric chains and their fit to the electron density. The red, orange, yellow and green segments of the lower bar indicate the fraction of residues that contain outliers for >=3, 2, 1 and 0 types of geometric quality criteria respectively. A grey segment represents the fraction of residues that are not modelled. The numeric value for each fraction is indicated below the corresponding segment, with a dot representing fractions <=5% The upper red bar (where present) indicates the fraction of residues that have poor fit to the electron density. The numeric value is given above the bar.

Mol	Chain	Length	Quality of chain
1	A	128	3% 91% 9%
1	B	128	5% 89% 11%
1	C	128	3% 89% 9%
1	D	128	9% 95%
1	E	128	4% 87% 12%

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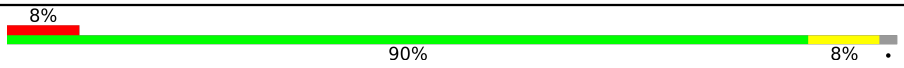
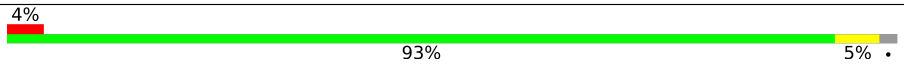
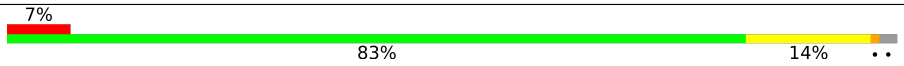
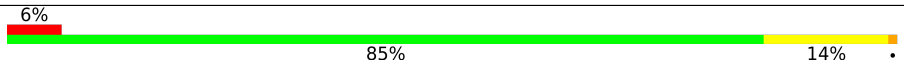
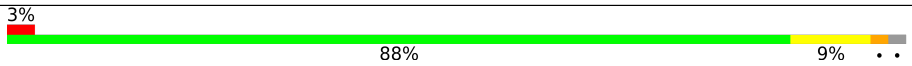
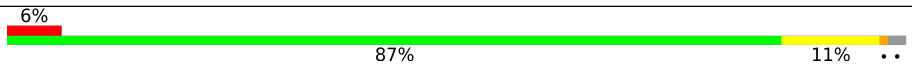
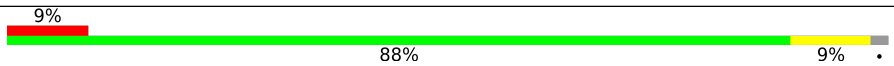
Mol	Chain	Length	Quality of chain
1	F	128	
1	G	128	
1	H	128	
1	I	128	
1	J	128	
1	K	128	
1	L	128	

2 Entry composition

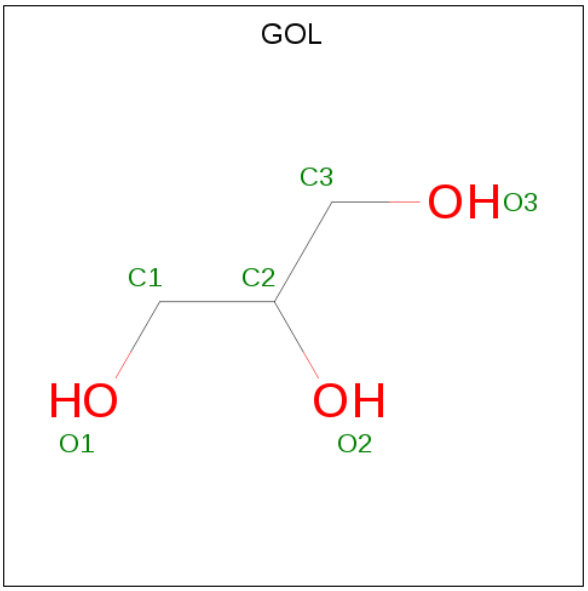
There are 3 unique types of molecules in this entry. The entry contains 14833 atoms, of which 8 are hydrogens and 0 are deuteriums.

In the tables below, the ZeroOcc column contains the number of atoms modelled with zero occupancy, the AltConf column contains the number of residues with at least one atom in alternate conformation and the Trace column contains the number of residues modelled with at most 2 atoms.

- Molecule 1 is a protein called RNase 3/1 version 1.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
1	G	125	Total	C	N	O	S	0	6	0
			1080	669	213	185	13			
1	J	126	Total	C	N	O	S	0	4	0
			1061	658	206	185	12			
1	C	126	Total	C	N	O	S	0	10	0
			1119	693	222	192	12			
1	D	126	Total	C	N	O	S	0	1	0
			1037	643	202	181	11			
1	E	126	Total	C	N	O	S	0	3	0
			1053	652	205	184	12			
1	F	125	Total	C	N	O	S	0	3	0
			1053	656	205	182	10			
1	A	128	Total	C	N	O	S	0	5	0
			1082	671	210	190	11			
1	H	125	Total	C	N	O	S	0	5	0
			1073	668	208	186	11			
1	I	128	Total	C	N	O	S	0	7	0
			1103	681	218	193	11			
1	B	128	Total	C	N	O	S	0	6	0
			1097	680	213	193	11			
1	L	125	Total	C	N	O	S	0	2	0
			1043	648	204	180	11			
1	K	126	Total	C	N	O	S	0	3	0
			1055	657	205	182	11			

- Molecule 2 is GLYCEROL (three-letter code: GOL) (formula: $C_3H_8O_3$).



Mol	Chain	Residues	Atoms	ZeroOcc	AltConf
2	A	1	Total C H O 14 3 8 3	0	0

- Molecule 3 is water.

Mol	Chain	Residues	Atoms	ZeroOcc	AltConf
3	G	179	Total O 179 179	0	0
3	J	157	Total O 157 157	0	0
3	C	146	Total O 146 146	0	0
3	D	154	Total O 154 154	0	0
3	E	167	Total O 167 167	0	0
3	F	151	Total O 151 151	0	0
3	A	182	Total O 182 182	0	0
3	H	163	Total O 163 163	0	0
3	I	173	Total O 173 173	0	0
3	B	171	Total O 171 171	0	0
3	L	143	Total O 143 143	0	0

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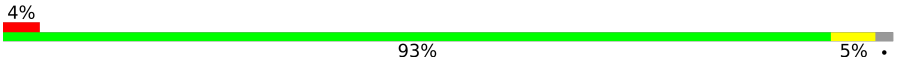
Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
3	K	177	Total 177	O 177	0	0

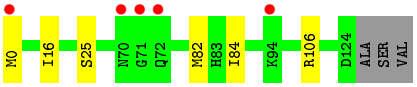
3 Residue-property plots (i)

These plots are drawn for all protein, RNA, DNA and oligosaccharide chains in the entry. The first graphic for a chain summarises the proportions of the various outlier classes displayed in the second graphic. The second graphic shows the sequence view annotated by issues in geometry and electron density. Residues are color-coded according to the number of geometric quality criteria for which they contain at least one outlier: green = 0, yellow = 1, orange = 2 and red = 3 or more. A red dot above a residue indicates a poor fit to the electron density (RSRZ > 2). Stretches of 2 or more consecutive residues without any outlier are shown as a green connector. Residues present in the sample, but not in the model, are shown in grey.

- Molecule 1: RNase 3/1 version 1

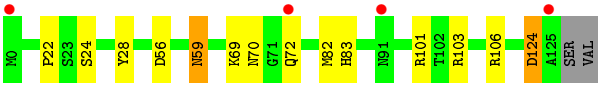
Chain G:





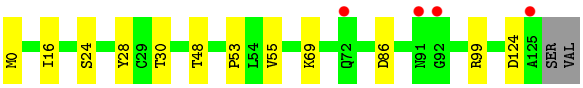
- Molecule 1: RNase 3/1 version 1

Chain J:



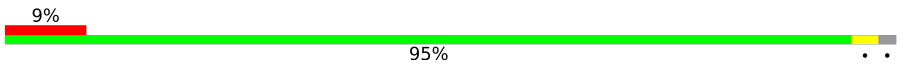
- Molecule 1: RNase 3/1 version 1

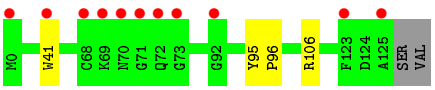
Chain C:



- Molecule 1: RNase 3/1 version 1

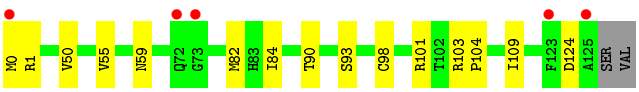
Chain D:





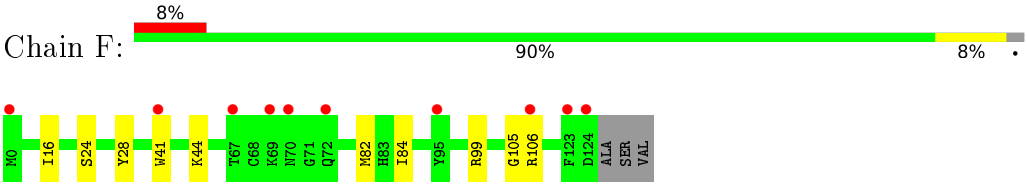
- Molecule 1: RNase 3/1 version 1

Chain E:



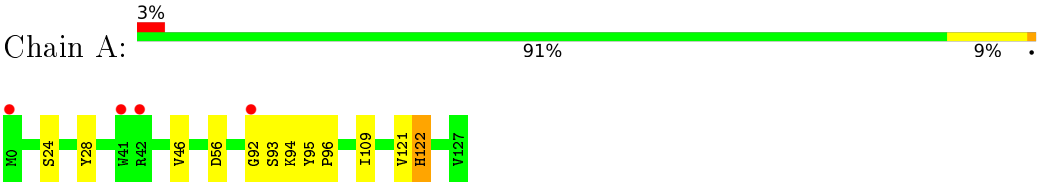
- Molecule 1: RNase 3/1 version 1

Chain F:



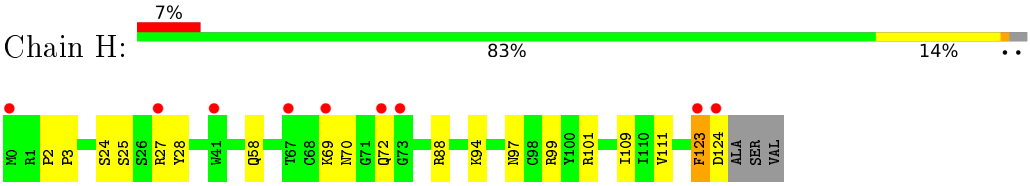
• Molecule 1: RNase 3/1 version 1

Chain A:



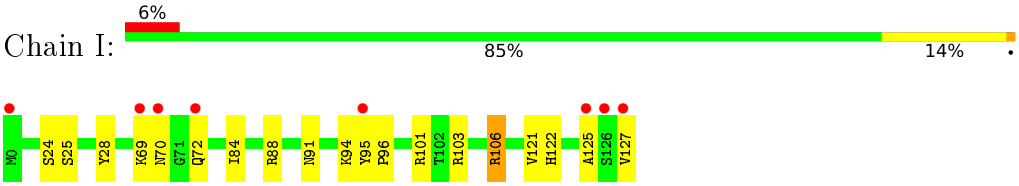
• Molecule 1: RNase 3/1 version 1

Chain H:



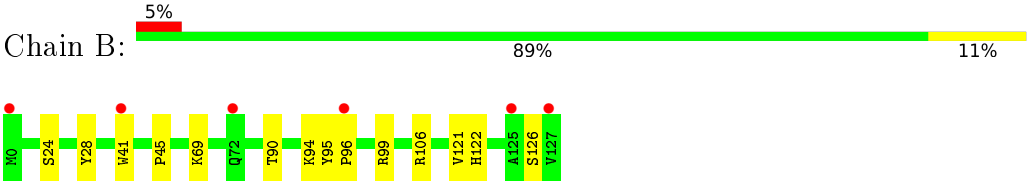
• Molecule 1: RNase 3/1 version 1

Chain I:



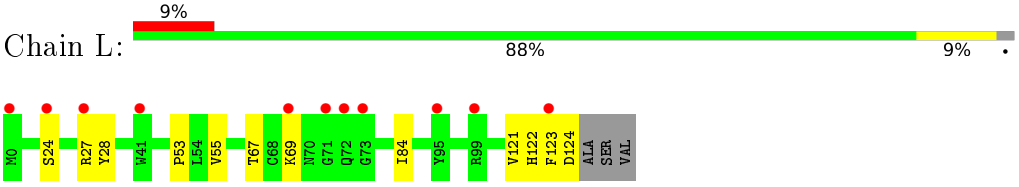
• Molecule 1: RNase 3/1 version 1

Chain B:



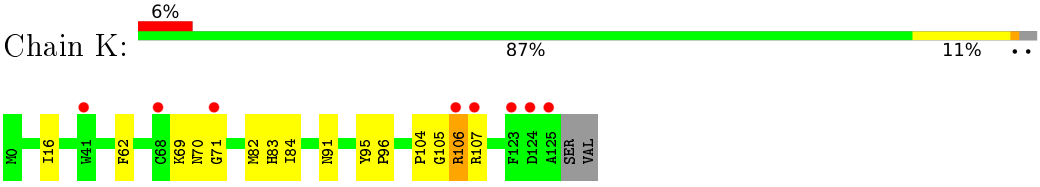
• Molecule 1: RNase 3/1 version 1

Chain L:



• Molecule 1: RNase 3/1 version 1

Chain K:



4 Data and refinement statistics (i)

Property	Value	Source
Space group	C 2 2 21	Depositor
Cell constants a, b, c, α, β, γ	106.84Å 115.68Å 284.74Å 90.00° 90.00° 90.00°	Depositor
Resolution (Å)	71.19 – 1.58 142.37 – 1.56	Depositor EDS
% Data completeness (in resolution range)	99.9 (71.19-1.58) 95.1 (142.37-1.56)	Depositor EDS
R_{merge}	(Not available)	Depositor
R_{sym}	(Not available)	Depositor
$< I/\sigma(I) >$ [1]	1.38 (at 1.56Å)	Xtriage
Refinement program	PHENIX 1.17.1_3660, PHENIX 1.17.1_3660	Depositor
R, R_{free}	0.178 , 0.203 0.178 , 0.203	Depositor DCC
R_{free} test set	11869 reflections (4.80%)	wwPDB-VP
Wilson B-factor (Å^2)	19.6	Xtriage
Anisotropy	0.259	Xtriage
Bulk solvent k_{sol}(e/Å^3), B_{sol}(Å^2)	0.35 , 51.3	EDS
L-test for twinning[2]	$< \|L\| > = 0.49$, $< L^2 > = 0.32$	Xtriage
Estimated twinning fraction	No twinning to report.	Xtriage
F_o,F_c correlation	0.97	EDS
Total number of atoms	14833	wwPDB-VP
Average B, all atoms (Å^2)	31.0	wwPDB-VP

Xtriage's analysis on translational NCS is as follows: *The largest off-origin peak in the Patterson function is 7.46% of the height of the origin peak. No significant pseudotranslation is detected.*

[1] Intensities estimated from amplitudes.

[2] Theoretical values of $< |L| >$, $< L^2 >$ for acentric reflections are 0.5, 0.333 respectively for untwinned datasets, and 0.375, 0.2 for perfectly twinned datasets.

5 Model quality

5.1 Standard geometry

Bond lengths and bond angles in the following residue types are not validated in this section: GOL

The Z score for a bond length (or angle) is the number of standard deviations the observed value is removed from the expected value. A bond length (or angle) with $|Z| > 5$ is considered an outlier worth inspection. RMSZ is the root-mean-square of all Z scores of the bond lengths (or angles).

Mol	Chain	Bond lengths		Bond angles	
		RMSZ	#$\|Z\|>5$	RMSZ	#$\|Z\|>5$
1	A	0.47	0/1112	0.65	0/1506
1	B	0.54	1/1127 (0.1%)	0.65	0/1524
1	C	0.36	0/1149	0.55	0/1554
1	D	0.47	0/1066	0.65	0/1443
1	E	0.49	0/1082	0.61	0/1464
1	F	0.56	0/1084	0.63	0/1470
1	G	0.45	0/1109	0.60	0/1498
1	H	0.58	0/1102	0.66	0/1492
1	I	0.59	0/1133	0.68	0/1534
1	J	0.58	0/1090	0.66	0/1475
1	K	0.40	0/1084	0.65	0/1467
1	L	0.52	0/1073	0.66	0/1453
All	All	0.51	1/13211 (0.0%)	0.64	0/17880

All (1) bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
1	B	106	ARG	C-N	-5.57	1.21	1.34

There are no bond angle outliers.

There are no chirality outliers.

There are no planarity outliers.

5.2 Too-close contacts

In the following table, the Non-H and H(model) columns list the number of non-hydrogen atoms and hydrogen atoms in the chain respectively. The H(added) column lists the number of hydrogen atoms added and optimized by MolProbity. The Clashes column lists the number of clashes within the asymmetric unit, whereas Symm-Clashes lists symmetry-related clashes.

Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
1	A	1082	0	1040	8	0
1	B	1097	0	1054	11	0
1	C	1119	0	1079	9	0
1	D	1037	0	996	9	0
1	E	1053	0	1009	11	0
1	F	1053	0	1004	8	0
1	G	1080	0	1044	6	0
1	H	1073	0	1040	14	0
1	I	1103	0	1060	25	0
1	J	1061	0	1019	17	0
1	K	1055	0	1022	17	0
1	L	1043	0	1001	15	0
2	A	6	8	8	1	0
3	A	182	0	0	1	0
3	B	171	0	0	1	0
3	C	146	0	0	4	0
3	D	154	0	0	1	0
3	E	167	0	0	4	0
3	F	151	0	0	1	0
3	G	179	0	0	1	0
3	H	163	0	0	2	0
3	I	173	0	0	2	0
3	J	157	0	0	1	0
3	K	177	0	0	5	0
3	L	143	0	0	1	0
All	All	14825	8	12376	133	0

The all-atom clashscore is defined as the number of clashes found per 1000 atoms (including hydrogen atoms). The all-atom clashscore for this structure is 5.

All (133) close contacts within the same asymmetric unit are listed below, sorted by their clash magnitude.

Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:J:83:HIS:CD2	1:J:106:ARG:HD3	1.91	1.05
1:J:83:HIS:CD2	1:J:106:ARG:CD	2.50	0.94
1:I:94:LYS:HE3	1:B:41:TRP:HE1	1.43	0.82
1:D:41:TRP:HB2	1:L:27:ARG:HD3	1.59	0.82
1:D:41:TRP:CB	1:L:27:ARG:HD3	2.16	0.75
1:K:104:PRO:HD2	3:K:248:HOH:O	1.87	0.74
1:D:41:TRP:CG	1:L:27:ARG:HD3	2.23	0.74
1:K:91:ASN:ND2	3:K:201:HOH:O	2.21	0.73
1:I:101[B]:ARG:NH1	1:I:103:ARG:HH21	1.88	0.72

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:C:48[B]:THR:HG22	1:C:86:ASP:OD1	1.89	0.72
1:L:69:LYS:HG2	1:L:124:ASP:OD1	1.92	0.70
1:H:123:PHE:O	1:H:124:ASP:OD1	2.09	0.69
1:J:83:HIS:CG	1:J:106:ARG:HD2	2.30	0.67
1:F:82:MET:O	1:F:106:ARG:HA	1.94	0.67
1:E:93[B]:SER:OG	1:E:98:CYS:HA	1.94	0.67
1:I:69:LYS:HB2	1:I:125:ALA:O	1.95	0.66
1:C:69:LYS:HG2	1:C:124:ASP:OD2	1.95	0.66
1:J:56:ASP:OD2	1:E:59[A]:ASN:ND2	2.28	0.65
1:I:95:TYR:CG	1:I:96:PRO:HA	2.31	0.65
1:J:83:HIS:CD2	1:J:106:ARG:HD2	2.32	0.64
3:I:313:HOH:O	1:B:94:LYS:HE3	1.98	0.64
1:I:95:TYR:CD1	1:I:96:PRO:HA	2.33	0.63
1:G:0[A]:MET:HG2	1:K:71:GLY:O	1.99	0.62
1:I:94:LYS:CE	1:B:41:TRP:HE1	2.13	0.60
1:H:69[B]:LYS:HD2	1:H:69[B]:LYS:H	1.66	0.60
1:I:94:LYS:HE3	1:B:41:TRP:NE1	2.16	0.60
1:K:16:ILE:HG23	3:K:209:HOH:O	2.01	0.59
1:K:83:HIS:NE2	1:K:106:ARG:HD2	2.18	0.59
1:E:103:ARG:HG2	3:E:222:HOH:O	2.02	0.59
1:I:101[B]:ARG:HH11	1:I:103:ARG:HD3	1.68	0.59
1:C:16:ILE:HG23	3:C:207:HOH:O	2.03	0.58
1:B:90[B]:THR:HG22	1:B:99:ARG:O	2.03	0.58
1:D:41:TRP:CG	1:L:27:ARG:CD	2.87	0.58
1:I:24:SER:HB3	1:I:28:TYR:HB2	1.86	0.57
1:I:106:ARG:NH2	3:I:202:HOH:O	2.29	0.57
1:A:95:TYR:CG	1:A:96:PRO:HA	2.39	0.57
1:I:101[B]:ARG:HH12	1:I:103:ARG:HG3	1.69	0.57
1:I:127:VAL:HG12	1:I:127:VAL:O	2.05	0.57
1:I:69:LYS:HD3	1:I:125:ALA:HB3	1.85	0.57
1:C:24:SER:HB3	1:C:28:TYR:HB2	1.88	0.56
1:J:83:HIS:CG	1:J:106:ARG:CD	2.88	0.55
1:J:83:HIS:HA	1:J:106:ARG:HD2	1.88	0.55
1:H:111:VAL:HG12	1:H:123:PHE:CD1	2.42	0.55
1:K:84[A]:ILE:HG13	1:K:105:GLY:O	2.07	0.55
1:H:69[B]:LYS:HD2	1:H:69[B]:LYS:N	2.21	0.55
1:J:59:ASN:ND2	1:A:56:ASP:OD2	2.29	0.55
1:C:55[B]:VAL:HG23	3:C:275:HOH:O	2.07	0.55
1:B:69:LYS:HA	1:B:126:SER:O	2.07	0.55
1:H:24:SER:HB3	1:H:28:TYR:HB2	1.88	0.54
1:J:70[A]:ASN:OD1	1:J:72:GLN:N	2.38	0.54

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:K:82:MET:O	1:K:106:ARG:HA	2.08	0.54
1:I:95:TYR:CE2	1:I:96:PRO:HB3	2.43	0.54
1:I:101[B]:ARG:NH1	1:I:103:ARG:HD3	2.22	0.54
1:I:101[B]:ARG:HH12	1:I:103:ARG:HH21	1.55	0.54
1:C:30:THR:HG21	1:C:99:ARG:HH21	1.73	0.53
1:F:84:ILE:HG13	1:F:105:GLY:O	2.09	0.53
1:K:84[B]:ILE:HG12	1:K:105:GLY:O	2.10	0.52
1:I:101[B]:ARG:NH1	1:I:103:ARG:CG	2.72	0.52
1:C:0:MET:SD	1:L:67:THR:HG21	2.49	0.52
1:I:70:ASN:ND2	1:I:72:GLN:HB2	2.25	0.52
1:D:95:TYR:CG	1:D:96:PRO:HA	2.44	0.52
1:H:88:ARG:HD3	1:H:101:ARG:NH2	2.25	0.52
1:G:0[A]:MET:HE3	1:K:70:ASN:O	2.09	0.52
1:E:90:THR:HG22	1:E:101:ARG:NH2	2.24	0.52
1:J:83:HIS:NE2	1:J:106:ARG:HD3	2.22	0.51
1:F:16:ILE:HG23	3:F:203:HOH:O	2.10	0.51
1:H:94:LYS:HE3	3:H:249:HOH:O	2.08	0.51
1:B:41:TRP:HD1	3:B:328:HOH:O	1.93	0.51
1:F:24:SER:HB3	1:F:28:TYR:HB2	1.93	0.50
1:K:84[B]:ILE:HD11	1:K:107:ARG:NH1	2.27	0.50
1:I:101[B]:ARG:NH1	1:I:103:ARG:HG3	2.27	0.49
1:K:82:MET:N	1:K:107:ARG:O	2.44	0.49
1:G:0[A]:MET:HE2	1:G:0[A]:MET:HA	1.95	0.49
1:L:55[B]:VAL:HG23	3:L:272:HOH:O	2.12	0.48
1:J:82[B]:MET:O	1:J:106:ARG:HA	2.13	0.48
1:D:95:TYR:CE2	1:D:96:PRO:HB3	2.48	0.48
1:E:55:VAL:HG23	3:E:265:HOH:O	2.13	0.48
1:H:25:SER:OG	1:H:27:ARG:HG2	2.13	0.48
1:I:88:ARG:HD2	1:I:101[B]:ARG:NH2	2.28	0.48
1:I:84:ILE:C	1:I:84:ILE:HD12	2.33	0.48
1:J:24:SER:HB3	1:J:28:TYR:HB2	1.96	0.48
1:F:41[B]:TRP:O	1:F:41[B]:TRP:CG	2.67	0.48
1:A:93:SER:C	1:A:94:LYS:HG3	2.34	0.48
1:H:70:ASN:ND2	1:H:72:GLN:HB2	2.30	0.47
1:J:101:ARG:HD2	1:J:103:ARG:NH1	2.29	0.47
1:H:97:ASN:OD1	1:H:99:ARG:NH1	2.48	0.47
1:L:24:SER:HB3	1:L:28:TYR:HB2	1.96	0.47
1:K:95:TYR:CG	1:K:96:PRO:HA	2.50	0.46
1:L:121:VAL:O	1:L:122[B]:HIS:HB3	2.15	0.46
1:E:50:VAL:HG11	1:E:82[B]:MET:HE2	1.98	0.46
1:D:41:TRP:CD1	1:L:27:ARG:HG2	2.50	0.46

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:L:24:SER:HB3	1:L:28:TYR:CB	2.46	0.46
1:B:95:TYR:CG	1:B:96:PRO:HA	2.51	0.45
1:C:53:PRO:HB3	3:C:322:HOH:O	2.15	0.45
1:H:58:GLN:HB3	3:H:203:HOH:O	2.17	0.45
1:K:107:ARG:HD3	3:K:204:HOH:O	2.17	0.45
1:F:41[B]:TRP:O	1:F:41[B]:TRP:CD1	2.70	0.44
1:L:53:PRO:HD3	1:K:62:PHE:CE2	2.53	0.44
1:A:92:GLY:O	1:A:94:LYS:HG3	2.17	0.44
1:B:24:SER:HB3	1:B:28:TYR:HB2	2.00	0.44
1:I:121:VAL:O	1:I:122[A]:HIS:HB3	2.18	0.44
1:E:84:ILE:C	1:E:84:ILE:HD12	2.39	0.43
1:F:84:ILE:C	1:F:84:ILE:HD12	2.39	0.43
1:K:107:ARG:HB2	3:K:300:HOH:O	2.18	0.43
1:G:16:ILE:HG23	3:G:206:HOH:O	2.18	0.43
1:E:0:MET:HE2	1:E:1:ARG:N	2.33	0.43
1:H:70:ASN:HD21	1:H:72:GLN:HB2	1.82	0.43
1:B:121:VAL:O	1:B:122[A]:HIS:HB3	2.18	0.43
1:E:104:PRO:HD2	3:E:239:HOH:O	2.18	0.43
1:E:50:VAL:HG11	1:E:82[B]:MET:CE	2.49	0.43
1:L:84:ILE:C	1:L:84:ILE:HD12	2.38	0.43
1:D:41:TRP:CD2	1:L:27:ARG:NE	2.75	0.43
1:A:121:VAL:O	1:A:122[B]:HIS:HB3	2.19	0.42
1:I:101[B]:ARG:NH1	1:I:103:ARG:CD	2.83	0.42
1:H:2:PRO:HA	1:H:3:PRO:HD3	1.96	0.42
1:A:46[B]:VAL:HG12	3:A:332:HOH:O	2.19	0.42
1:D:41:TRP:HB3	3:D:229:HOH:O	2.19	0.42
1:H:109:ILE:HD12	1:H:123:PHE:HE1	1.85	0.42
1:L:122[A]:HIS:CD2	1:L:123:PHE:O	2.73	0.42
1:K:69[B]:LYS:N	1:K:69[B]:LYS:HD2	2.35	0.42
1:J:22:PRO:HG2	3:E:249:HOH:O	2.20	0.41
1:I:91:ASN:OD1	1:B:45:PRO:HD2	2.20	0.41
1:K:83:HIS:CD2	1:K:106:ARG:HG3	2.55	0.41
1:J:69:LYS:HG2	1:J:124:ASP:OD2	2.19	0.41
1:J:70[A]:ASN:ND2	3:J:204:HOH:O	2.54	0.41
1:J:70[A]:ASN:O	1:F:44:LYS:HE3	2.20	0.41
1:G:84:ILE:HD12	1:G:84:ILE:C	2.40	0.41
1:G:82[B]:MET:O	1:G:106:ARG:HA	2.21	0.41
1:A:24:SER:HB3	1:A:28:TYR:HB2	2.01	0.41
1:I:24:SER:HB3	1:I:28:TYR:CB	2.50	0.41
1:E:82[B]:MET:HG3	1:E:109:ILE:HG12	2.02	0.41
1:A:109:ILE:HG22	2:A:201:GOL:H2	2.03	0.40

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:C:55[A]:VAL:HG13	3:C:275:HOH:O	2.21	0.40

There are no symmetry-related clashes.

5.3 Torsion angles

5.3.1 Protein backbone

In the following table, the Percentiles column shows the percent Ramachandran outliers of the chain as a percentile score with respect to all X-ray entries followed by that with respect to entries of similar resolution.

The Analysed column shows the number of residues for which the backbone conformation was analysed, and the total number of residues.

Mol	Chain	Analysed	Favoured	Allowed	Outliers	Percentiles	
1	A	131/128 (102%)	129 (98%)	2 (2%)	0	100	100
1	B	132/128 (103%)	128 (97%)	4 (3%)	0	100	100
1	C	134/128 (105%)	130 (97%)	4 (3%)	0	100	100
1	D	125/128 (98%)	121 (97%)	4 (3%)	0	100	100
1	E	127/128 (99%)	125 (98%)	2 (2%)	0	100	100
1	F	126/128 (98%)	123 (98%)	3 (2%)	0	100	100
1	G	128/128 (100%)	126 (98%)	2 (2%)	0	100	100
1	H	129/128 (101%)	126 (98%)	3 (2%)	0	100	100
1	I	133/128 (104%)	129 (97%)	4 (3%)	0	100	100
1	J	128/128 (100%)	126 (98%)	2 (2%)	0	100	100
1	K	127/128 (99%)	125 (98%)	2 (2%)	0	100	100
1	L	125/128 (98%)	120 (96%)	5 (4%)	0	100	100
All	All	1545/1536 (101%)	1508 (98%)	37 (2%)	0	100	100

There are no Ramachandran outliers to report.

5.3.2 Protein sidechains

In the following table, the Percentiles column shows the percent sidechain outliers of the chain as a percentile score with respect to all X-ray entries followed by that with respect to entries of similar

resolution.

The Analysed column shows the number of residues for which the sidechain conformation was analysed, and the total number of residues.

Mol	Chain	Analysed	Rotameric	Outliers	Percentiles
1	A	122/117 (104%)	120 (98%)	2 (2%)	62 39
1	B	123/117 (105%)	123 (100%)	0	100 100
1	C	125/117 (107%)	125 (100%)	0	100 100
1	D	116/117 (99%)	115 (99%)	1 (1%)	78 64
1	E	118/117 (101%)	117 (99%)	1 (1%)	81 68
1	F	117/117 (100%)	116 (99%)	1 (1%)	78 64
1	G	121/117 (103%)	120 (99%)	1 (1%)	81 68
1	H	121/117 (103%)	120 (99%)	1 (1%)	81 68
1	I	124/117 (106%)	121 (98%)	3 (2%)	49 22
1	J	119/117 (102%)	117 (98%)	2 (2%)	60 36
1	K	118/117 (101%)	117 (99%)	1 (1%)	81 68
1	L	117/117 (100%)	117 (100%)	0	100 100
All	All	1441/1404 (103%)	1428 (99%)	13 (1%)	81 64

All (13) residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
1	G	25	SER
1	J	59	ASN
1	J	124	ASP
1	D	106	ARG
1	E	124	ASP
1	F	99	ARG
1	A	122[A]	HIS
1	A	122[B]	HIS
1	H	123	PHE
1	I	25[A]	SER
1	I	25[B]	SER
1	I	106	ARG
1	K	106	ARG

Sometimes sidechains can be flipped to improve hydrogen bonding and reduce clashes. There are no such sidechains identified.

5.3.3 RNA

There are no RNA molecules in this entry.

5.4 Non-standard residues in protein, DNA, RNA chains

There are no non-standard protein/DNA/RNA residues in this entry.

5.5 Carbohydrates

There are no monosaccharides in this entry.

5.6 Ligand geometry

1 ligand is modelled in this entry.

In the following table, the Counts columns list the number of bonds (or angles) for which Mogul statistics could be retrieved, the number of bonds (or angles) that are observed in the model and the number of bonds (or angles) that are defined in the Chemical Component Dictionary. The Link column lists molecule types, if any, to which the group is linked. The Z score for a bond length (or angle) is the number of standard deviations the observed value is removed from the expected value. A bond length (or angle) with $|Z| > 2$ is considered an outlier worth inspection. RMSZ is the root-mean-square of all Z scores of the bond lengths (or angles).

Mol	Type	Chain	Res	Link	Bond lengths			Bond angles		
					Counts	RMSZ	$\#\|Z\| > 2$	Counts	RMSZ	$\#\|Z\| > 2$
2	GOL	A	201	-	5,5,5	0.23	0	5,5,5	0.35	0

In the following table, the Chirals column lists the number of chiral outliers, the number of chiral centers analysed, the number of these observed in the model and the number defined in the Chemical Component Dictionary. Similar counts are reported in the Torsion and Rings columns. '-' means no outliers of that kind were identified.

Mol	Type	Chain	Res	Link	Chirals	Torsions	Rings
2	GOL	A	201	-	-	0/4/4/4	-

There are no bond length outliers.

There are no bond angle outliers.

There are no chirality outliers.

There are no torsion outliers.

There are no ring outliers.

1 monomer is involved in 1 short contact:

Mol	Chain	Res	Type	Clashes	Symm-Clashes
2	A	201	GOL	1	0

5.7 Other polymers

There are no such residues in this entry.

5.8 Polymer linkage issues

There are no chain breaks in this entry.

6 Fit of model and data

6.1 Protein, DNA and RNA chains

In the following table, the column labelled '#RSRZ> 2' contains the number (and percentage) of RSRZ outliers, followed by percent RSRZ outliers for the chain as percentile scores relative to all X-ray entries and entries of similar resolution. The OWAB column contains the minimum, median, 95^{th} percentile and maximum values of the occupancy-weighted average B-factor per residue. The column labelled 'Q< 0.9' lists the number of (and percentage) of residues with an average occupancy less than 0.9.

Mol	Chain	Analysed	<RSRZ>	#RSRZ>2	OWAB(Å^2)	Q<0.9
1	A	128/128 (100%)	-0.16	4 (3%) 49 50	17, 23, 52, 59	1 (0%)
1	B	128/128 (100%)	-0.15	6 (4%) 31 31	18, 23, 47, 59	0
1	C	126/128 (98%)	-0.10	4 (3%) 47 49	16, 27, 55, 65	0
1	D	126/128 (98%)	0.16	11 (8%) 10 10	17, 25, 67, 81	1 (0%)
1	E	126/128 (98%)	0.00	5 (3%) 38 39	17, 25, 54, 80	0
1	F	125/128 (97%)	0.09	10 (8%) 12 12	17, 25, 57, 100	0
1	G	125/128 (97%)	-0.10	5 (4%) 38 39	17, 23, 46, 88	0
1	H	125/128 (97%)	0.06	9 (7%) 15 15	18, 25, 56, 84	0
1	I	128/128 (100%)	0.14	8 (6%) 20 20	18, 25, 62, 87	0
1	J	126/128 (98%)	-0.02	4 (3%) 47 49	16, 25, 54, 80	0
1	K	126/128 (98%)	0.15	8 (6%) 20 20	17, 25, 54, 83	0
1	L	125/128 (97%)	0.10	11 (8%) 10 9	18, 26, 63, 97	0
All	All	1514/1536 (98%)	0.02	85 (5%) 24 24	16, 25, 57, 100	2 (0%)

All (85) RSRZ outliers are listed below:

Mol	Chain	Res	Type	RSRZ
1	K	125	ALA	17.6
1	I	127	VAL	14.7
1	J	125	ALA	6.6
1	F	41[A]	TRP	6.5
1	I	125	ALA	6.5
1	C	125	ALA	6.3
1	F	72	GLN	6.3
1	A	41	TRP	5.7
1	D	41	TRP	5.5
1	E	125	ALA	5.5
1	B	127	VAL	5.3

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Mol	Chain	Res	Type	RSRZ
1	H	41	TRP	5.1
1	K	41	TRP	4.9
1	L	41	TRP	4.7
1	K	68	CYS	4.7
1	G	72	GLN	4.6
1	K	124	ASP	4.6
1	D	92	GLY	4.5
1	D	70	ASN	4.3
1	E	73	GLY	4.2
1	E	72	GLN	4.1
1	I	126	SER	4.1
1	L	0	MET	4.0
1	J	0	MET	3.9
1	H	123	PHE	3.9
1	H	72	GLN	3.9
1	I	95	TYR	3.9
1	J	72	GLN	3.9
1	H	0	MET	3.8
1	B	41	TRP	3.7
1	F	123	PHE	3.7
1	D	72	GLN	3.6
1	F	69	LYS	3.5
1	D	69	LYS	3.2
1	C	91	ASN	3.2
1	D	71	GLY	3.2
1	D	73	GLY	3.1
1	D	123	PHE	3.1
1	L	72	GLN	3.1
1	H	73	GLY	3.0
1	G	70	ASN	3.0
1	D	125	ALA	3.0
1	F	70	ASN	3.0
1	I	72	GLN	2.9
1	G	71	GLY	2.9
1	D	68	CYS	2.9
1	F	67	THR	2.8
1	L	27	ARG	2.8
1	K	123	PHE	2.8
1	A	0	MET	2.8
1	I	0	MET	2.7
1	K	107	ARG	2.7
1	C	72	GLN	2.7

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Mol	Chain	Res	Type	RSRZ
1	E	0	MET	2.7
1	F	0	MET	2.7
1	L	71	GLY	2.7
1	I	69	LYS	2.6
1	J	91	ASN	2.6
1	A	42	ARG	2.6
1	B	0	MET	2.5
1	F	95	TYR	2.5
1	L	24	SER	2.4
1	L	69	LYS	2.4
1	G	94	LYS	2.3
1	G	0[A]	MET	2.3
1	E	123	PHE	2.3
1	H	124	ASP	2.3
1	H	27	ARG	2.3
1	H	67	THR	2.3
1	K	106	ARG	2.3
1	B	96	PRO	2.2
1	I	70	ASN	2.2
1	B	125	ALA	2.2
1	C	92	GLY	2.2
1	L	95	TYR	2.2
1	F	106	ARG	2.2
1	L	123	PHE	2.1
1	L	99	ARG	2.1
1	A	92	GLY	2.1
1	H	69[A]	LYS	2.1
1	L	73	GLY	2.1
1	K	71	GLY	2.1
1	D	0	MET	2.0
1	B	72	GLN	2.0
1	F	124	ASP	2.0

6.2 Non-standard residues in protein, DNA, RNA chains (i)

There are no non-standard protein/DNA/RNA residues in this entry.

6.3 Carbohydrates (i)

There are no monosaccharides in this entry.

6.4 Ligands

In the following table, the Atoms column lists the number of modelled atoms in the group and the number defined in the chemical component dictionary. The B-factors column lists the minimum, median, 95^{th} percentile and maximum values of B factors of atoms in the group. The column labelled 'Q< 0.9' lists the number of atoms with occupancy less than 0.9.

Mol	Type	Chain	Res	Atoms	RSCC	RSR	B-factors(Å^2)	Q<0.9
2	GOL	A	201	6/6	0.94	0.10	28,39,47,47	0

6.5 Other polymers

There are no such residues in this entry.